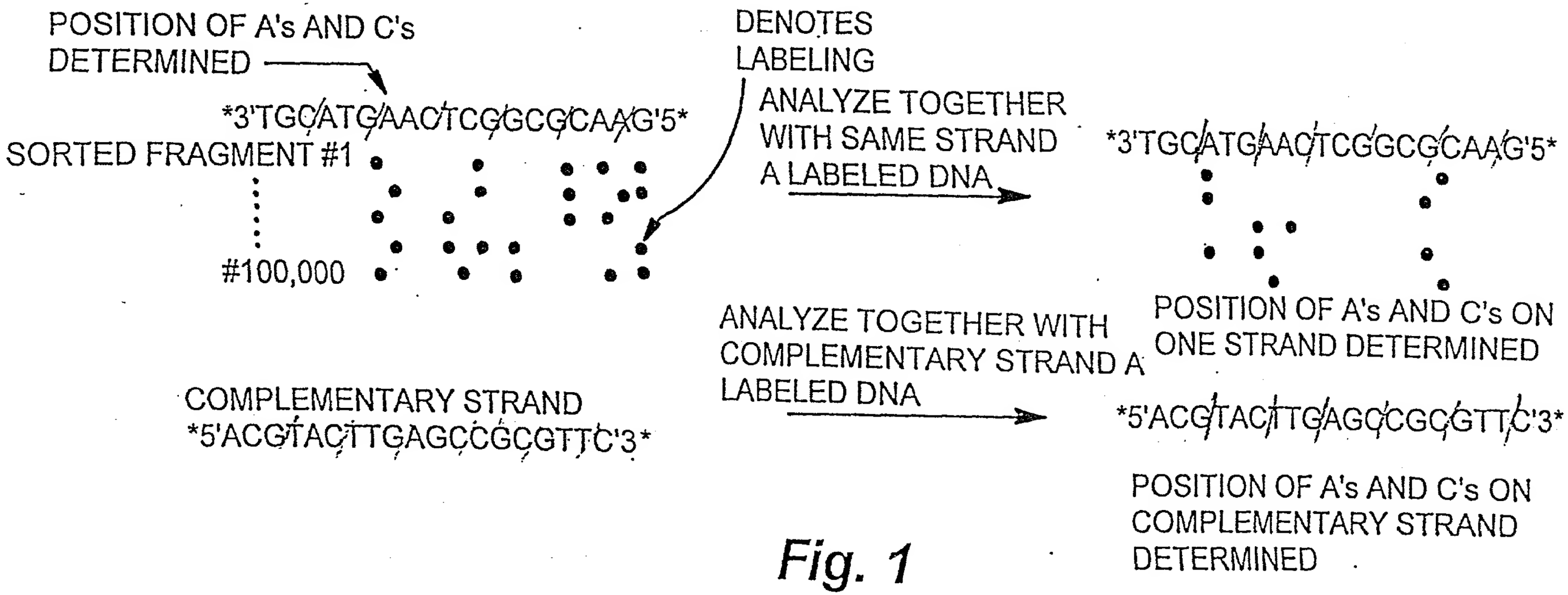


Fig. 1

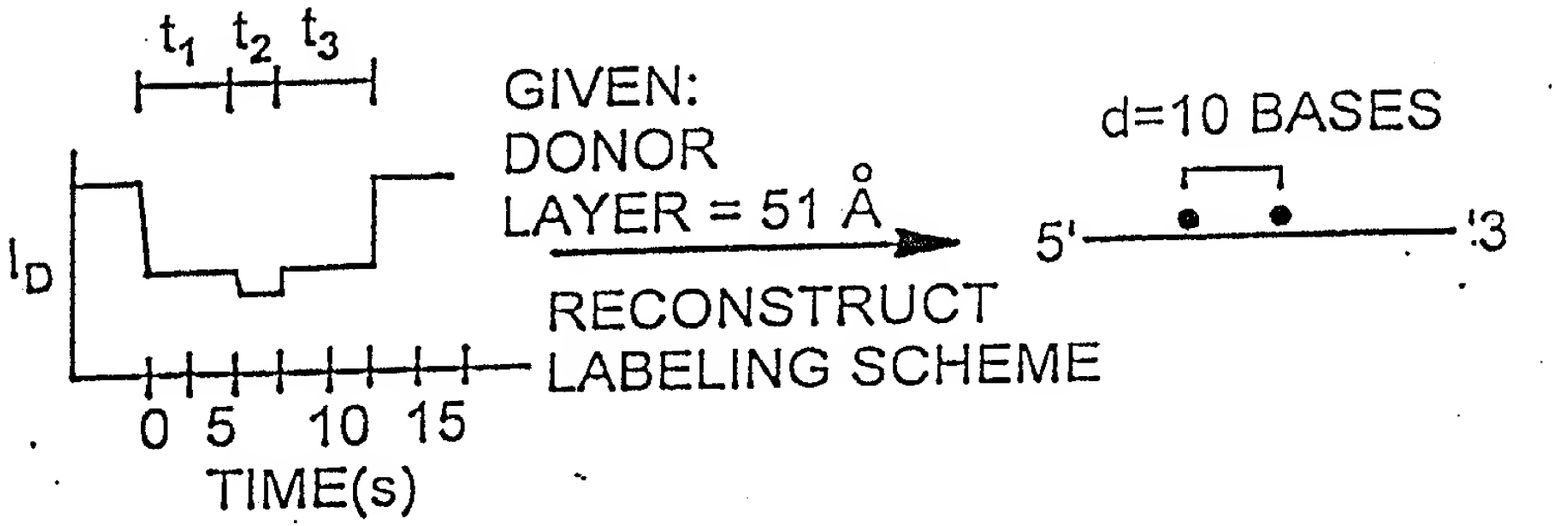

t_1 t_2 t_3
GIVEN:
DONOR
LAYER = 51 Å
d=10 BASES
5'
3'
I_D
RECONSTRUCT
LABELING SCHEME
0 5 10 15
TIME(s)

Fig. 2

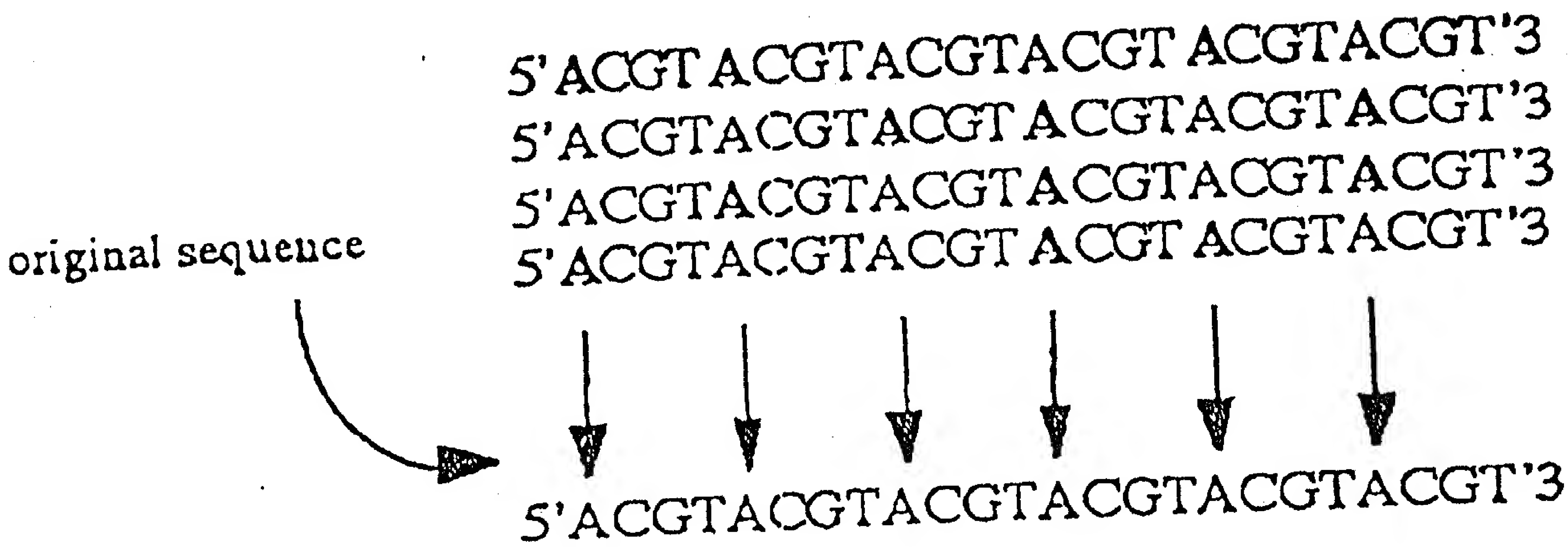
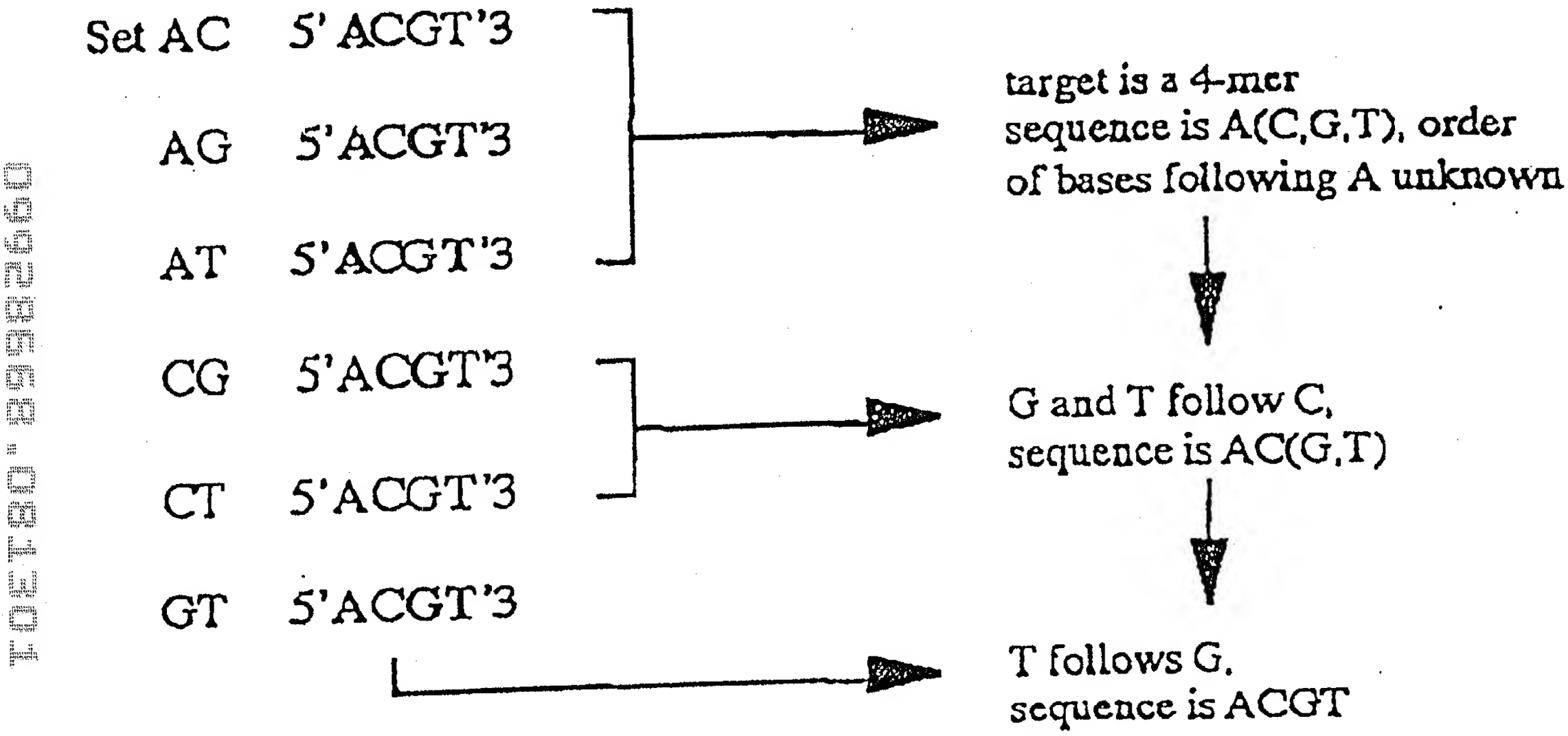
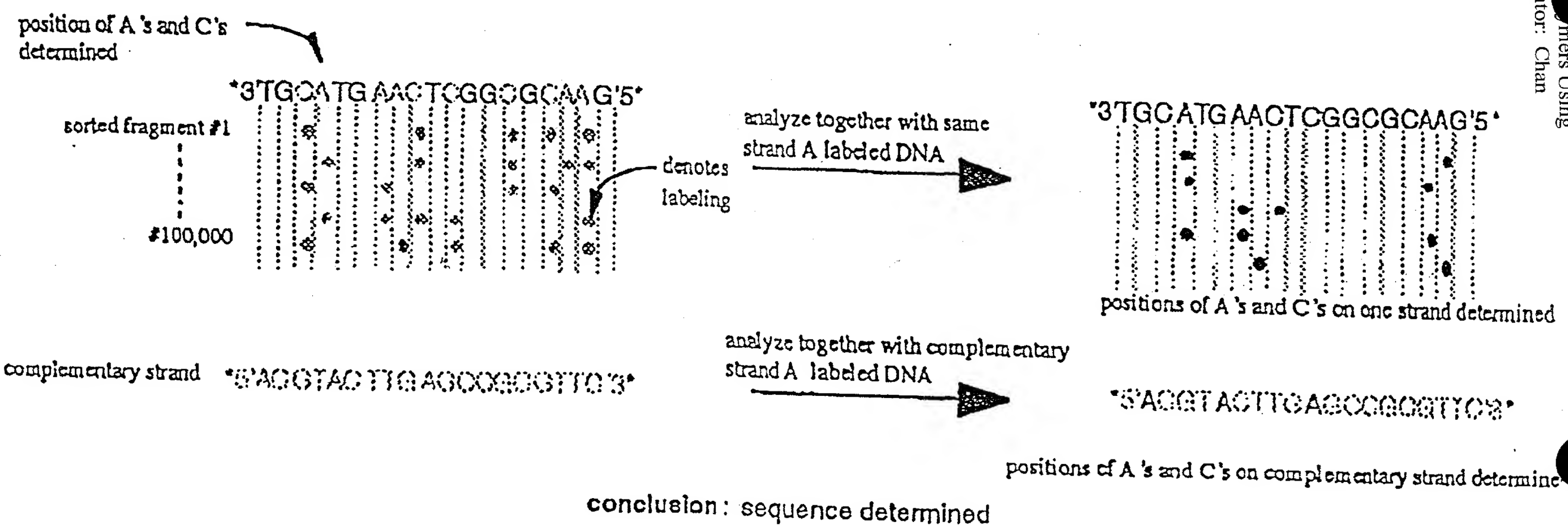

5'ACGTACGTACGTACGTACGTACGT'3
5'ACGTACGTACGTACGTACGTACGT'3
5'ACGTACGTACGTACGTACGTACGT'3
5'ACGTACGTACGTACGTACGTACGT'3
original sequence
5'ACGTACGTACGTACGTACGTACGT'3

FIGURE 3



Two base labeling and analysis.

FIGURE 4



Sorted fragments are used to reconstruct the sequence of the DNA. Using population analysis, the position of the A's and C's on one strand a termined. Subsequently, the position of all the A's on the same strand are determined using the same method. In a similar fashion, the positiions of the nd C's on the complementary strand give information about the G's and T's of the first strand analyzed. The sequence can thus be reconstructed.

FIGURE 5

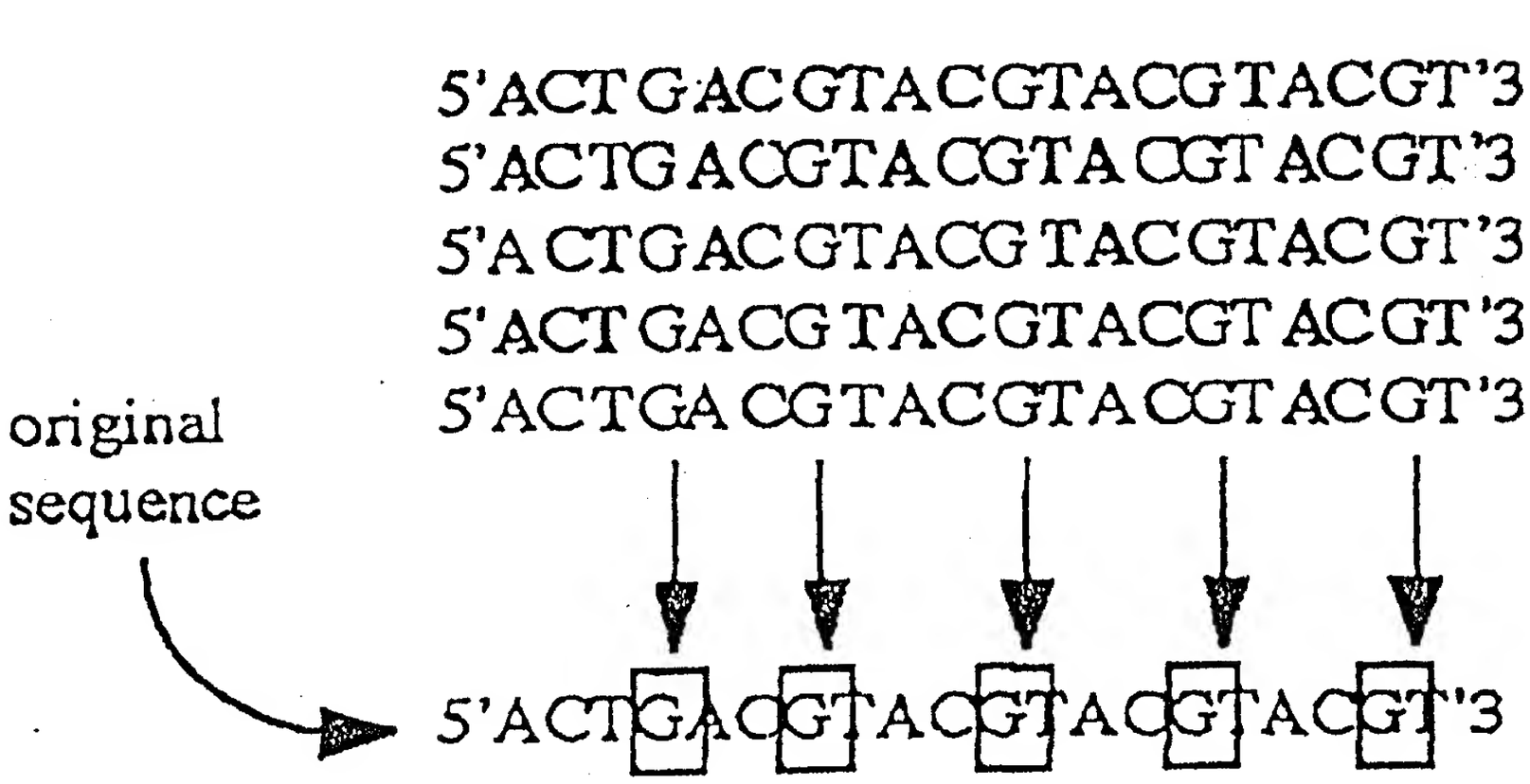
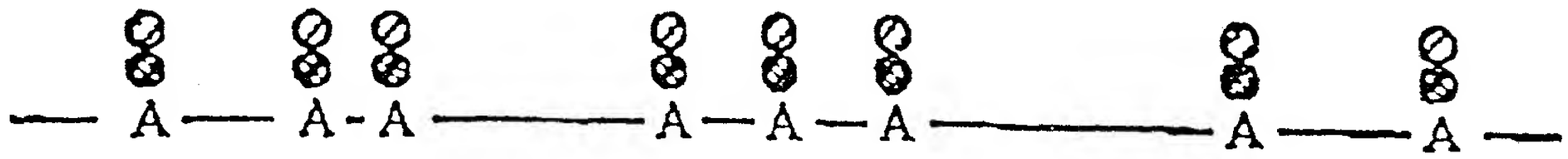

5'ACTGACGTACGTACGTACGT'3
5'ACTGACGTACGTACGTACGT'3
5'ACTGACGTACGTACGTACGT'3
5'ACTGACGTACGTACGTACGT'3
5'ACTGACGTACGTACGTACGT'3
original
sequence
5'ACTGACGTACGTACGTACGT'3

FIGURE 6

scheme of dual labeling of individual bases



dual characteristic labeled 'A'

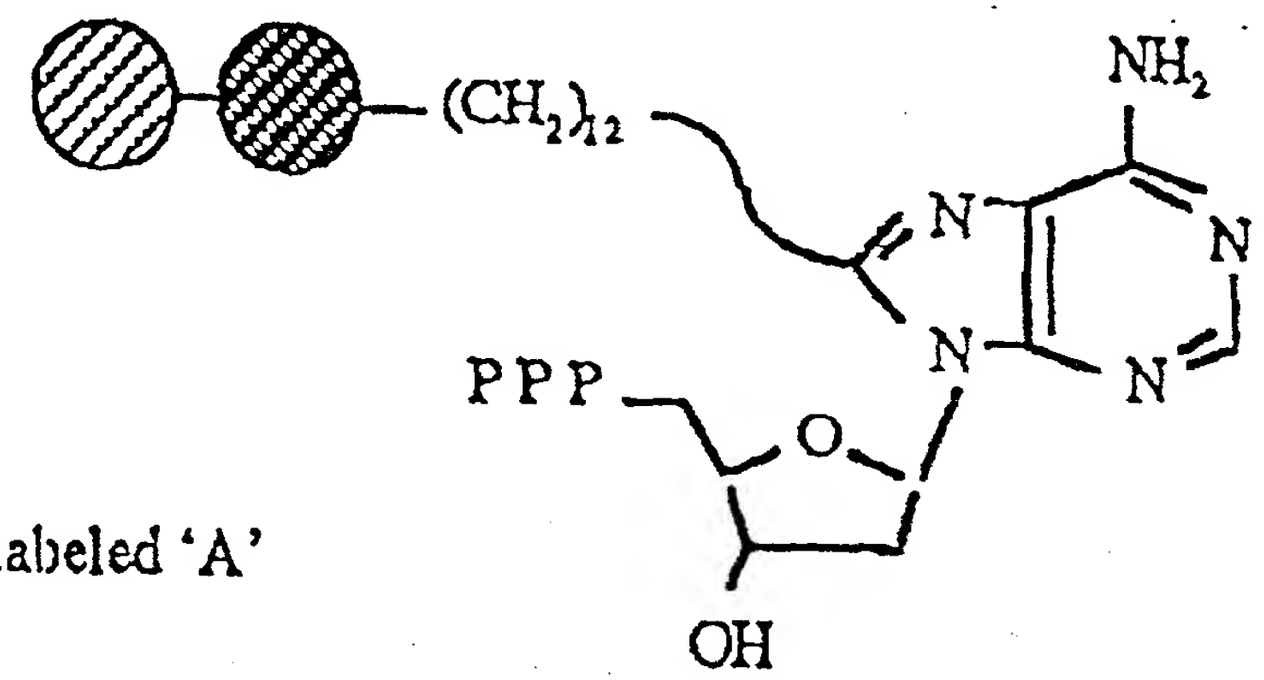


FIGURE 7

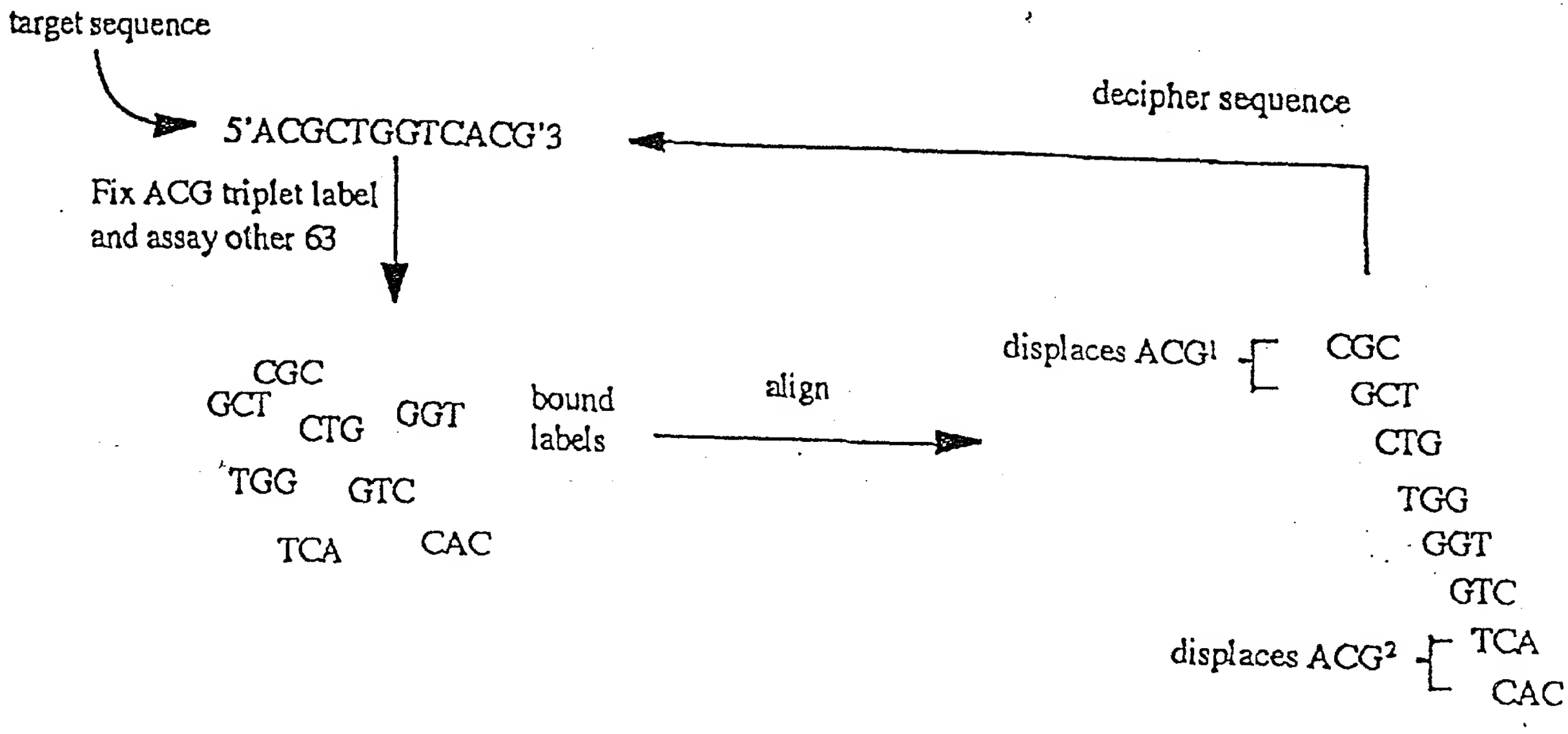
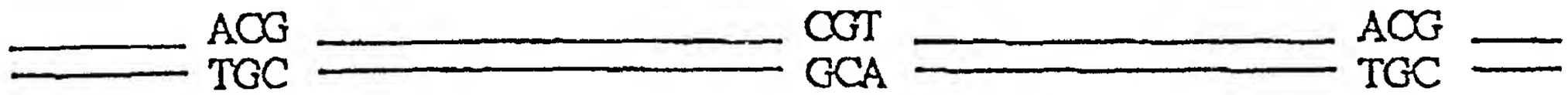


FIGURE 8

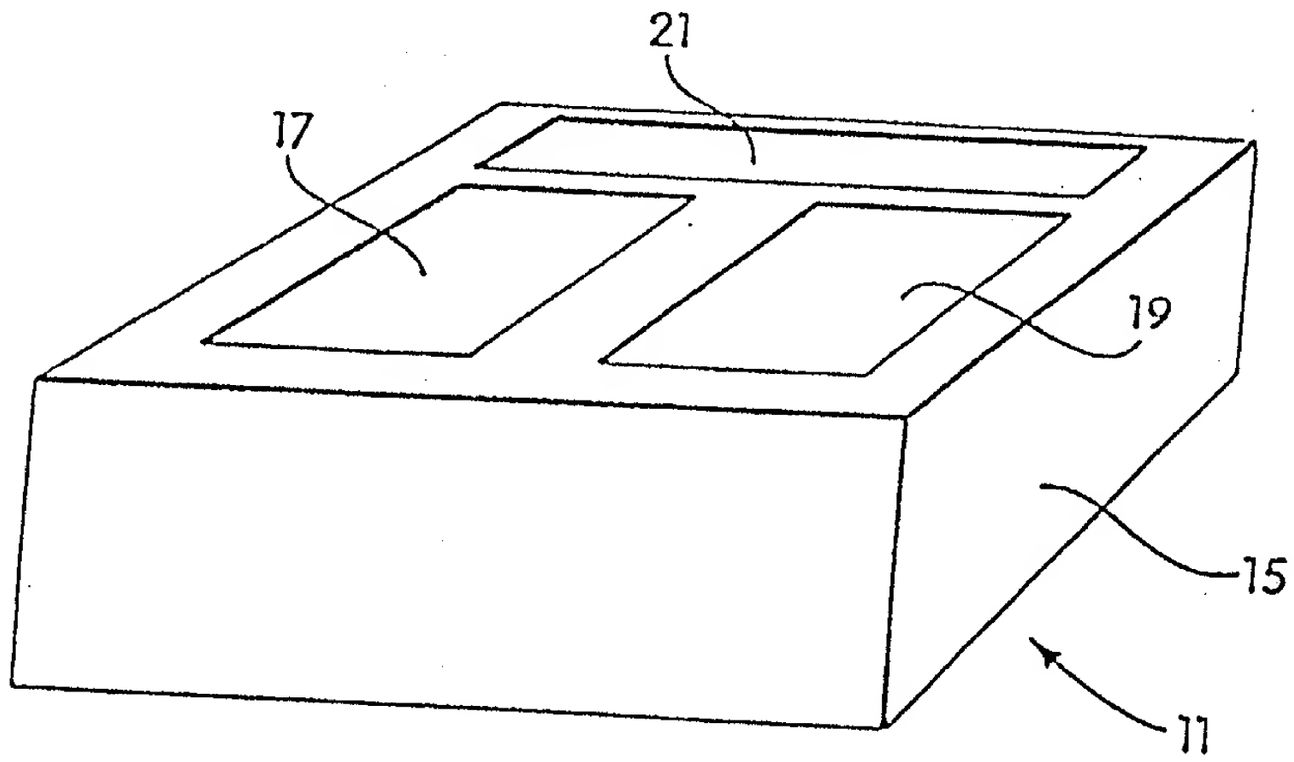


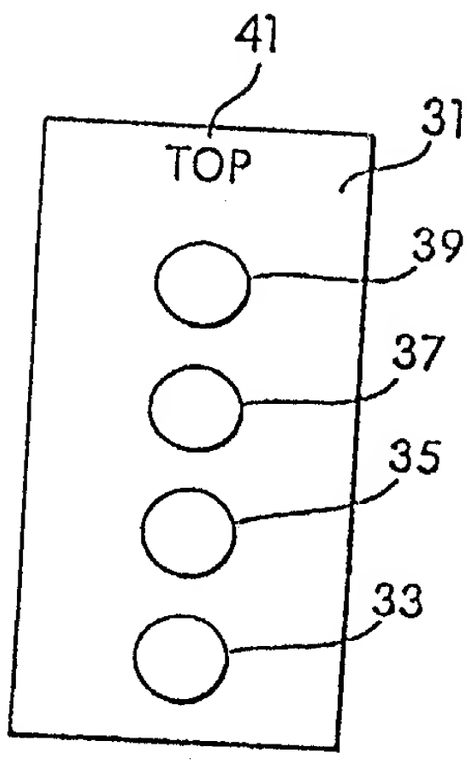
direction non-specific binders

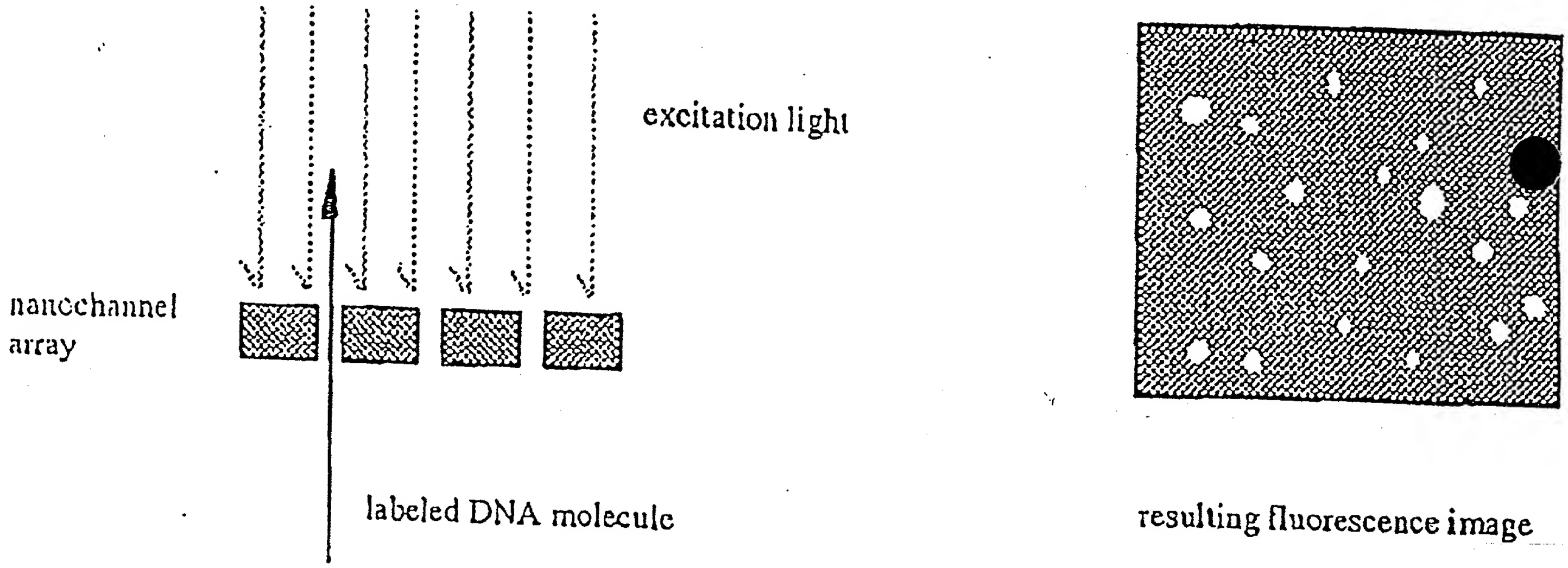
direction specific labels

FIGURE 9

Figure 10

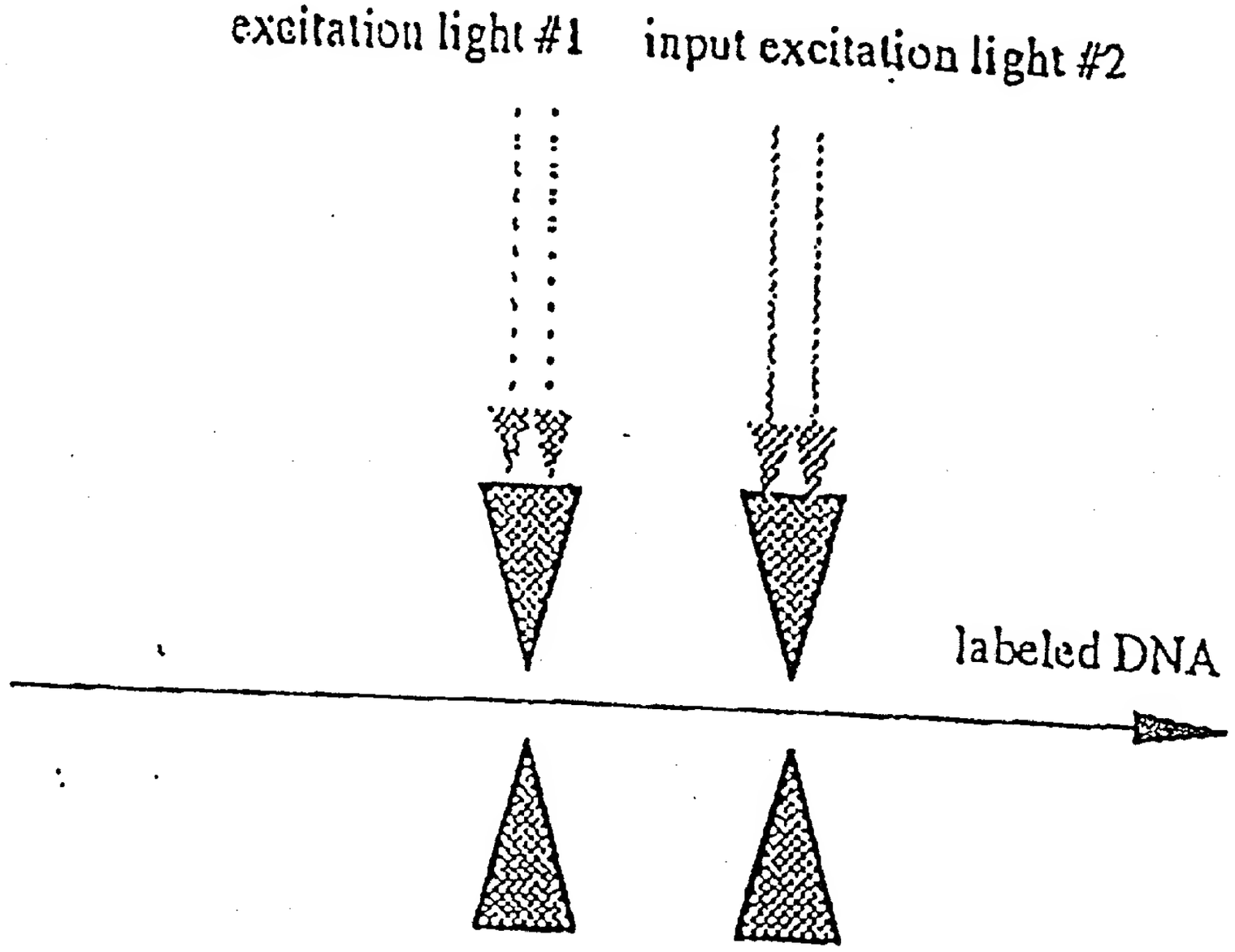


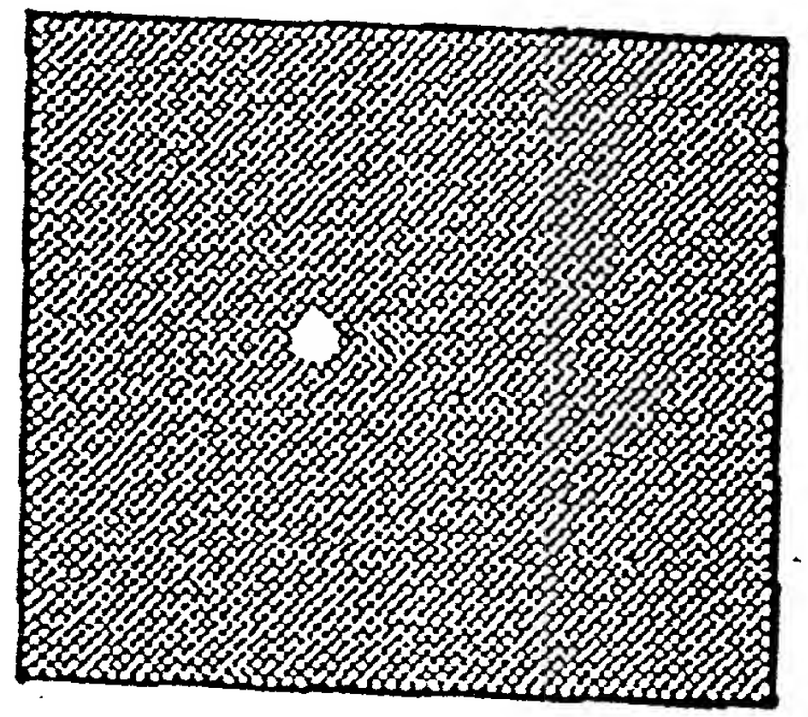




Example 1 and migration of DNA through nanochannel plate.

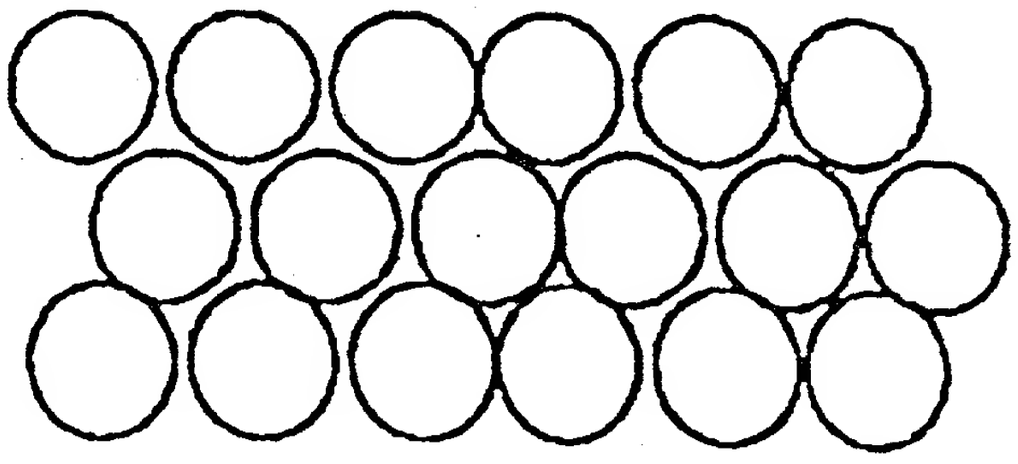
FIGURE 11

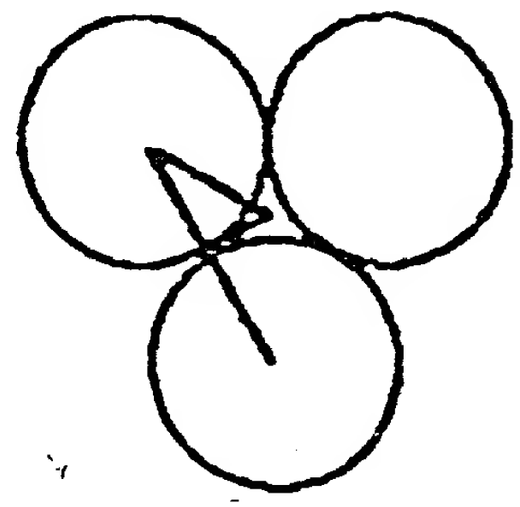




resulting fluorescence image

FIGURE 12





Example 3 of hexagonally packed beads as restrictive nanostructures.

FIGURE 13